

REMARKS

I. Status of the Application

Claims 1, 2, 7-14, 18-25 and 37 are pending in the application. Claims 1, 2, 7-14, 18-25 and 37 stand rejected under 35 U.S.C. §112, first paragraph, as failing to comply with the written description requirement. Claims 1, 2, 7-14, 18-25 and 37 stand rejected under 35 U.S.C. §112, first paragraph, as lacking enablement. Claims 1, 2, 7-14, 18-25 and 37 stand rejected under 35 U.S.C. §112, second paragraph, as being indefinite.

Applicants have amended the claims to more clearly define and distinctly characterize Applicants' novel invention. Support for the amendments can be found in the specification and the claims as originally filed. Specifically, support for the amendments to claims 1, 2, 7 and 22 to recite "human lysophospholipase homolog HU-K5" can be found in the specification at least at Figure 7, page 8, where Applicants describe U67963 as human lysophospholipase homolog (HU-K5). The amendments presented herein add no new matter. Applicants respectfully request entry and consideration of the foregoing amendments, which are intended to place the case in condition for allowance.

Applicants respectfully submit that the amendments presented herein do not raise new issues requiring further search. The present Amendment and Response is being filed within 2 months of the mailing date of the Final Office Action, accordingly, Applicants request issuance of an advisory action.

II. Objections

At page 5, section 6 of the instant Office Action, the Examiner notes that the trademark GENBANK is used in the application and states that it should be capitalized whenever it appears, i.e., claims 1, 2, 7 and 22. Applicants respectfully submit that claims 1, 2, 7 and 22, as amended, no longer recite a GenBank Accession Number, thus rendering this objection moot.

III. The Specification Provides Adequate Written Description for Claims 1, 2, 7-14, 18-25 and 37

At page 2, section 3 of the instant Office Action, claims 1, 2, 7-14, 18-25 and 37 stand rejected under 35 U.S.C. §112, first paragraph, as failing to comply with the written description requirement. The Examiner is of the opinion that the claims contain subject matter that was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventors, at the time the application was filed, had possession of the claimed invention. The Examiner asserts that specifically, while the claims refer to GenBank Accession No. U67963, the specification does not actually recite the sequence that corresponded to the Accession No. at the time the instant invention was made. The Examiner is of the opinion that as database Accession entries are not fixed, but rather changeable over time, and that the recitation of this Accession No. in the claims does not convey to one of skill in the art the sequence actually possessed by Applicant at the time the invention was made. Applicants respectfully traverse this rejection.

Without acquiescing to this rejection, Applicants respectfully submit that claims 1, 2, 7 and 22 have been amended to replace “lysophospholipase-like having a GenBank Accession Number of U67963” with “human lysophospholipase homolog HU-K5.” Applicants respectfully

submit that one of skill in the art would readily understand that which Applicants claim, specifically, what is meant by human lysophospholipase homolog HU-K5, as this gene was known in the art at the time of filing. Applicants provide herewith the GeneCard for MGLL (monoglyceride lipase), which provides aliases for this gene and lists five additional names including lysophospholipase-like and human lysophospholipase homolog (HU-K5) (Attachment A). Thus, human lysophospholipase homolog HU-K5 is understood in the art. Given the knowledge in the art of the identity of human lysophospholipase homolog HU-K5 and Applicants' teaching that this gene is associated with oral cancer, one of skill in the art would understand that the specification sufficiently describes the claimed invention in view of the amended claims now presented.

Accordingly, the Examiner is respectfully requested to reconsider and withdraw the rejection of claims 1, 2, 7-14, 18-25 and 37 under 35 U.S.C. §112, first paragraph, as failing to comply with the written description requirement.

IV. Claims 1, 2, 7-14, 18-25 and 37 are Enabled

At page 3, section 4 of the instant Office Action, claims 1, 2, 7-14, 18-25 and 37 stand rejected under 35 U.S.C. §112, first paragraph, as lacking enablement. Applicants gratefully acknowledge that the Examiner has indicated that Applicants' arguments have overcome the instant rejection in part, i.e., with respect to monitoring the progression of cancer. With regard to "lysophospholipase-like," the Examiner is of the opinion that the specification does not recite the sequence that corresponded to Accession No. U67963 at that time, and concludes that the quantity of experimentation required to use the claimed invention is clearly undue. Applicants respectfully traverse this rejection in view of the amended claims now presented.

Applicants respectfully submit that amended claims 1, 2, 7 and 22, which recite “human lysophospholipase homolog HU-K5,” are enabled. As discussed above, the human lysophospholipase homolog HU-K5 described in the instant specification was known in the art at the time of filing. Indeed, the sequence was commercially available on an Affymetrix GeneChip at the time of filing (specification, page 22, lines 13-14 and Figure 7). Thus, Applicants’ specification, in view of the knowledge in the art at the time of filing, enables a person skilled in the art to make and use the claimed invention.

Accordingly, the Examiner is respectfully requested to reconsider and withdraw the rejection of claims 1, 2, 7-14, 18-25 and 37 under 35 U.S.C. §112, first paragraph, as lacking enablement.

V. Claims 1-2, 7-14, 18-25 and 37 Are Definite

At page 5, section 5 of the instant Office Action, claims 1-2, 7-14, 18-25 and 37 stand rejected under 35 U.S.C. §112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which Applicants regard as the invention. The Examiner is of the opinion that the recitation of an Accession Number in the claims renders them vague and indefinite, as the Accession Number does not provide a clear and definite structural description of the molecule of the claims. Applicants respectfully traverse this rejection in view of the amended claims now presented.

Applicants respectfully submit that the claims no longer recite an Accession Number, and that the term human lysophospholipase homolog HU-K5 is definite. Applicants submit that the

specification describes human lysophospholipase homolog HU-K5 at least at Figure 7, and that this gene was known in the art at the time of filing.

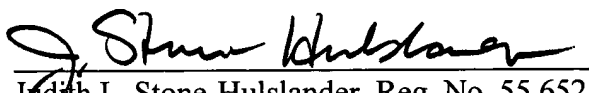
Accordingly, Applicants submit that claims 1, 2, 7 and 22 and claims depending therefrom are clear and definite because they reasonably convey to one skilled in the art what the invention is. Thus, Applicants respectfully request that the rejection of claims 1-2, 7-14, 18-25 and 37 under 35 U.S.C. §112, second paragraph, be reconsidered and withdrawn.

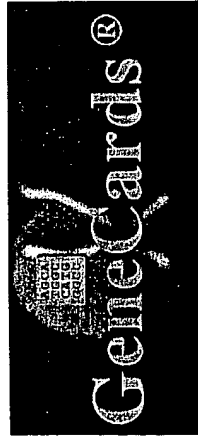
VI. Conclusion

Having addressed all outstanding issues, Applicants respectfully request reconsideration and allowance of the case. To the extent the Examiner believes that it would facilitate allowance of the case, the Examiner is requested to telephone the undersigned at the number below.

Respectfully submitted,

Dated: November 14, 2005


Judith L. Stone-Hulslander, Reg. No. 55,652
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(617) 720-9600



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GeneCard for gene **MGLL**

GC03M128731

Approved [UCL/HGNC/HUGO Human Gene Nomenclature database](#) symbol

MGLL (monoglyceride lipase)

Aliases and Descriptions

(According to [GDB](#),
[OMIM](#), [HUGO](#),
[LocusLink](#), [SWISS-
PROT](#)/[TrEMBL](#), and/or
[GeneLoc](#))

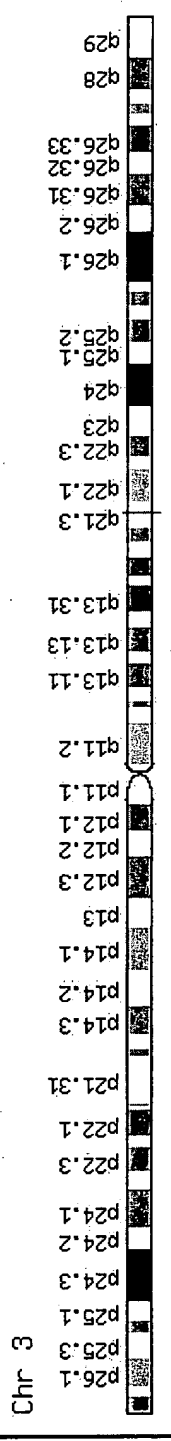
- HU-K5 (LL)
- MGL (LL)
- lysophospholipase-like (LL)
- Human lysophospholipase homolog (HU-K5) mRNA, complete cds (GDB)
- monoglyceride lipase (GDB, LL, HUGO)

Previous GC identifiers: GC03M124242 GC03M127569 GC03M128692

Chromosome: **3** [GeneLoc](#) gene densities

[LocusLink](#) cytogenetic band: **3q21.3** [Ensembl](#) cytogenetic band: **3q21.3**

Gene in genomic location: bands according to [Ensembl](#), locations according to [GeneLoc](#) (and/or [LocusLink](#) and/or [Ensembl](#) if c



Chromosomal Location

(According to [GeneLoc](#)
and/or [HUGO](#), and/or
[LocusLink](#) (NCBI build
34),

Genomic Views
According to [UCSC](#)
and [Ensembl](#))

[GeneLoc](#) location for GC03M128731: (about GC identifiers)

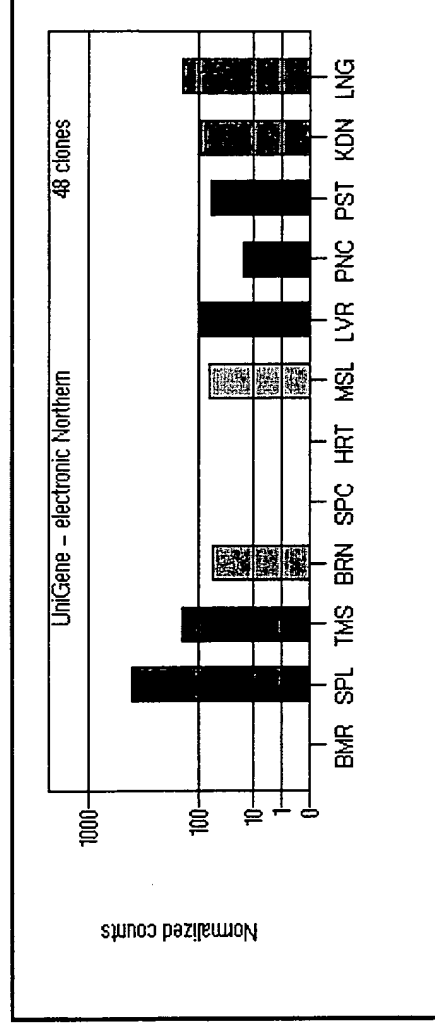
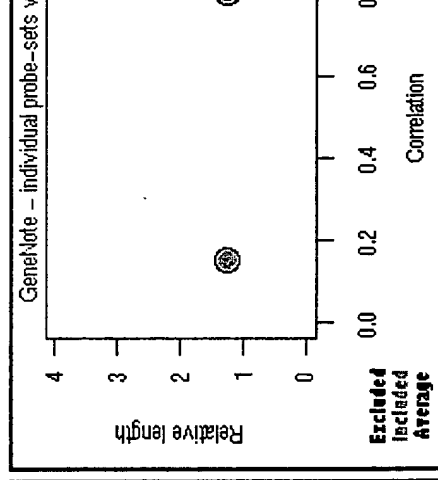
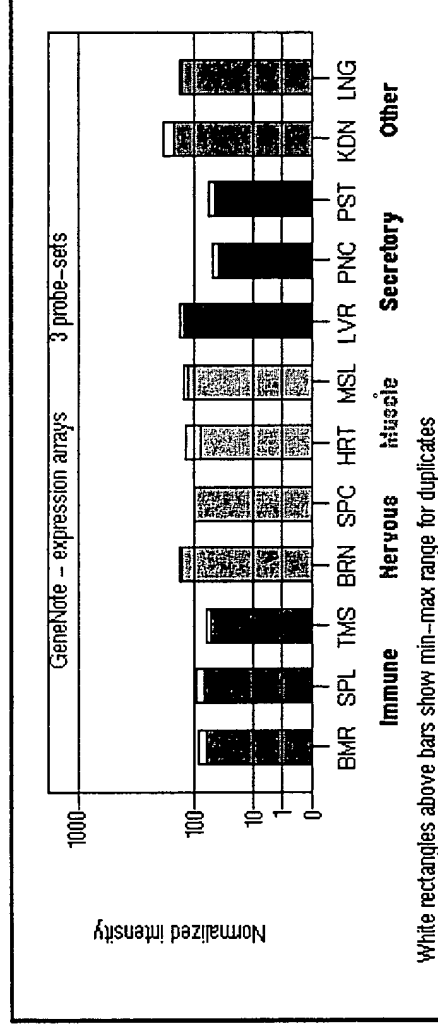
Start: **128,731,869 bp from pter**
End: **128,862,937 bp from pter**
Size: **131,068 bases**
Orientation: **minus strand**

Genomic View:

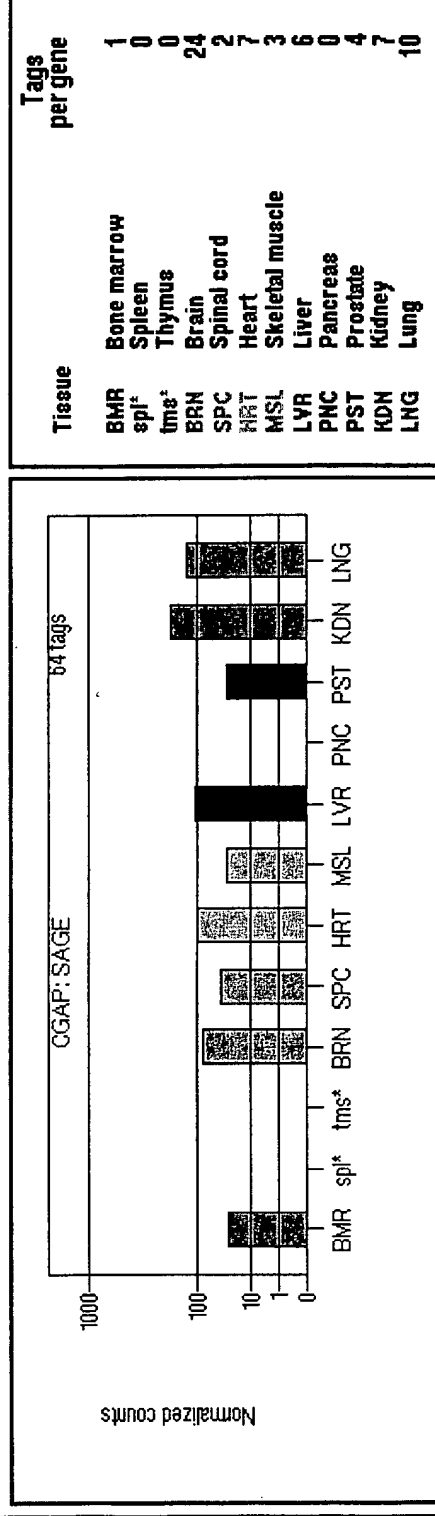
UCSC Golden Path with GeneCards custom track	
Proteins (According to SWISS-PROT/TrEMBL and/or MIPS, PDB rendering according to OCA)	MIPS Pedant Viewer: 62541 REFSEQ proteins: NP_009214.1
Protein Domains/Families (According to InterPro, ProNet, SWISS-PROT/TrEMBL, and/or BLOCKS)	-
Ontologies and Pathways (According to Gene Ontology Consortium Feb 2004, SWISS-PROT/TrEMBL, and KEGG)	Gene Ontology (GO) terms (links to tree view): GO:006725 aromatic compound metabolism GO:0066629 lipid metabolism GO:004622 lysophospholipase activity GO:006954 inflammatory response GO:0016787 hydrolase activity
Sequences (GenBank/EMBL/DDBJ Accessions According to Unigene (Build 166 Homo sapiens; Feb 16 2004) or GenBank, RefSeq According to LocusLink, Assembly According to MIPS, DOTS, and/or AceView)	REFSEQ mRNAs: NM_007283.4 Additional Gene/cDNA sequence: AF131821.1 AI125141.1 AJ270950.1 AK025983.1 AK091314.1 AK093841.1 AK125135.1 AL365376.1 AL833254.1 BC000551.2 BC006230.2 BC047298.1 BM051374.1 BM669411.1 BX640777.1 U67963.1 MIPS assembly: H53025S2 DOTS assembly: DT.451832 DT.100811512 DT.100045119 DT.91642727 DT.91824705 DT.40213558 DT.95351809 DT.40199175 DT.91741086 DT.97827256 DT.40107043 DT.91764633 DT.95256583 DT.97859396 DT.99989590 DT.100811509 AceView transcripts: List and properties of supporting cDNA sequences Unigene Cluster for MGLL: monoglyceride lipase Hs.409826 [show with all ESTs] Unigene Representative Sequence: NM_007283
	MGLL expression in normal human tissues according to GeneNote/GeneAnnot

Expression in Human Tissues
(Experimental results according to GeneNote, Annotation connecting genes to Affymetrix probe sets according to GeneAnnot, Electronic Northern calculations according to data from UniGene (Build 166 Homo sapiens), SAGE tags according to CGAP, plus additional links to SOURCE, and/or SWISS-PROT/TrEMBL)

Affymetrix probe-set	array	sensitivity	specificity	# of genes	correlation	relative length
70703 at	E	1	1	1	0.1524	1.2531
51988 at	B	1	1	1	0.8053	1.2659
35792 at	A	1	1	1	0.8894	0.5033



Tissue	Clones per gene
BMR	0
SPL	5
TMS	1
BRN	8
SPC	0
HRT	0
MSL	1
LVR	8
PNC	1
PST	4
KDN	6
LNG	14



CGAP SAGE TAG: GTCTGGGGGA

SOURCE GeneReport for Unigene cluster: Hs.409826

Homologues

	gene	locus	description	% similarity to human	NCBI accessions
rat (HomoloGene)	Mgll	--	monoglyceride lipase	83.33 (nucleic)	LocusLink:29254 NM_138502.1
mouse (MGD)	Mgll	6	monoglyceride lipase	--	syntenic AA589436 AJ001118 / AK006949 AK028008 BC03351
mouse (HomoloGene)	Mgll	--	monoglyceride lipase	82.55 (nucleic)	LocusLink:23945 NM_011844.3
zebrafish (HomoloGene)	zgc56561	--	hypothetical protein MGC56561	73.87 (nucleic)	LocusLink:393267 AY398382.1
tropical clawed frog (HomoloGene)	Str.4432	--	Transcribed sequence with weak similarity to protein refNP_009214.1 (H.sapiens) monoglyceride lipase; lysophospholipase-like; likely ortholog of mouse monoglyceride lipase [Homo sapiens]	70.47 (nucleic)	AL850963.2

No similarity-to-human data found for MGLL in HomoloGene for: pig, cow, African clawed frog, fruit fly, worm, sea squirt, green algae, tomato, barley, rice, wheat, corn, thale cress, medicago trunc, amoeba, chicken, soybean, rainbow trout, malaria parasite, loblolly pine, sorghum, baker's yeast, schistosoma parasite, sugarcane, fission yeast, toxoplasmosis, Alicante grape

Related Human Genes

(Pseudogenes according to pseudogene.org)	--																																																																																																																																																											
SNPs/Variants (According to the NCBI SNP Database and SWISS-PROT/TrEMBL)	NCBI SNPs: 10/261 selected, not withdrawn, single nucleotide mutations are shown here. Click here to see all of them																																																																																																																																																											
	<table><thead><tr><th colspan="7">Genomic Data</th><th colspan="5">Transcription Data</th></tr><tr><th>SNP ID</th><th>Contig Accession</th><th>Pos in Contig</th><th>Str</th><th>5' Flanking Sequence*</th><th>3' Flanking Sequence*</th><th>Validation</th><th>DNA Chg</th><th>AA Chg</th><th>Type</th><th>mRNA Accession</th><th>Protein Accession</th></tr></thead><tbody><tr><td>rs782080</td><td>NT_005612.14</td><td>33963815</td><td>+</td><td>TTTACTGTTT</td><td>agaggaggcc</td><td>by-cluster</td><td>A/T</td><td>--</td><td>intron</td><td>NM_007283</td><td>NP_0092</td></tr><tr><td>rs782081</td><td>NT_005612.14</td><td>33966384</td><td>-</td><td>gccgggcgtg</td><td>tggcttatgc</td><td>by-cluster</td><td>A/G</td><td>--</td><td>intron</td><td>NM_007283</td><td>NP_0092</td></tr><tr><td>rs782082</td><td>NT_005612.14</td><td>33966376</td><td>-</td><td>tgatggctta</td><td>gccgtgaatc</td><td>by-cluster</td><td>C/T</td><td>--</td><td>intron</td><td>NM_007283</td><td>NP_0092</td></tr><tr><td>rs6791406</td><td>NT_005612.14</td><td>33990305</td><td>+</td><td>gaatcacctc</td><td>tgtatctttt</td><td>by-2hit-2allele</td><td>A/G</td><td>--</td><td>intron</td><td>NM_007283</td><td>NP_0092</td></tr><tr><td>rs597956</td><td>NT_005612.14</td><td>33927713</td><td>-</td><td>GAAGATGGAC</td><td>GGCACCTCCA</td><td>by-frequency</td><td>C/T</td><td>--</td><td>intron</td><td>NM_007283</td><td>NP_0092</td></tr><tr><td>rs9869280</td><td>NT_005612.14</td><td>33989741</td><td>+</td><td>GCCGAGAGTG</td><td>GTGTTAGGAA</td><td>by-2hit-2allele</td><td>C/T</td><td>--</td><td>intron</td><td>NM_007283</td><td>NP_0092</td></tr><tr><td>rs584886</td><td>NT_005612.14</td><td>33927132</td><td>-</td><td>AATATCTAGA</td><td>GTGAGTTCTT</td><td>by-frequency</td><td>A/T</td><td>--</td><td>intron</td><td>NM_007283</td><td>NP_0092</td></tr><tr><td>rs7634643</td><td>NT_005612.14</td><td>33911967</td><td>+</td><td>TTCCTGCAGC</td><td>GGCCTGCTGC</td><td>by-2hit-2allele</td><td>A/G</td><td>--</td><td>intron</td><td>NM_007283</td><td>NP_0092</td></tr><tr><td>rs6766626</td><td>NT_005612.14</td><td>33990300</td><td>+</td><td>tataagaatc</td><td>cctcgtgat</td><td>by-2hit-2allele</td><td>A/C</td><td>--</td><td>intron</td><td>NM_007283</td><td>NP_0092</td></tr><tr><td>rs3817477</td><td>NT_005612.14</td><td>34036183</td><td>-</td><td>TCTTGCAGCT</td><td>GGTCTTTGTA</td><td>by-frequency</td><td>A/G</td><td>--</td><td>intron</td><td>NM_007283</td><td>NP_0092</td></tr></tbody></table>												Genomic Data							Transcription Data					SNP ID	Contig Accession	Pos in Contig	Str	5' Flanking Sequence*	3' Flanking Sequence*	Validation	DNA Chg	AA Chg	Type	mRNA Accession	Protein Accession	rs782080	NT_005612.14	33963815	+	TTTACTGTTT	agaggaggcc	by-cluster	A/T	--	intron	NM_007283	NP_0092	rs782081	NT_005612.14	33966384	-	gccgggcgtg	tggcttatgc	by-cluster	A/G	--	intron	NM_007283	NP_0092	rs782082	NT_005612.14	33966376	-	tgatggctta	gccgtgaatc	by-cluster	C/T	--	intron	NM_007283	NP_0092	rs6791406	NT_005612.14	33990305	+	gaatcacctc	tgtatctttt	by-2hit-2allele	A/G	--	intron	NM_007283	NP_0092	rs597956	NT_005612.14	33927713	-	GAAGATGGAC	GGCACCTCCA	by-frequency	C/T	--	intron	NM_007283	NP_0092	rs9869280	NT_005612.14	33989741	+	GCCGAGAGTG	GTGTTAGGAA	by-2hit-2allele	C/T	--	intron	NM_007283	NP_0092	rs584886	NT_005612.14	33927132	-	AATATCTAGA	GTGAGTTCTT	by-frequency	A/T	--	intron	NM_007283	NP_0092	rs7634643	NT_005612.14	33911967	+	TTCCTGCAGC	GGCCTGCTGC	by-2hit-2allele	A/G	--	intron	NM_007283	NP_0092	rs6766626	NT_005612.14	33990300	+	tataagaatc	cctcgtgat	by-2hit-2allele	A/C	--	intron	NM_007283	NP_0092	rs3817477	NT_005612.14	34036183	-	TCTTGCAGCT	GGTCTTTGTA	by-frequency	A/G	--	intron	NM_007283	NP_0092
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	* Lower case letters indicate repetitive or low-complexity sequence																																																																																																																																																											
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Disorders & Mutations (in which this Gene is Involved, According to OMIM, SWISS-PROT/TrEMBL, Genatlas, GeneTests, HGMD, GAD, BCGD, and/or TGDB.)	--																																																																																																																																																											

Medical News (Possibly Related Articles in <u>Doctor's</u> <u>Guide</u>)	-
Research Articles (in PubMed)	<ul style="list-style-type: none">• <u>A novel poxvirus gene and its human homolog are similar to an E. coli lysophospholipase.</u>
MGLL in Other Genome Wide Resources: (According to GDB, <u>LocusLink</u> , <u>AceView</u> , <u>euGenes</u> , <u>Ensembl</u> and/or <u>GeneLynx</u>)	<div><input type="text" value="Search PubMed for MGLL"/> to find abstracts of research articles containing this gene name</div> GDB: <u>9958022</u> <u>LocusLink: 11343</u> <u>AceView</u> <u>euGenes: HUgn11343</u> <u>Ensembl: ENSG00000074416</u>
MGLL in General Databases, Limited Scope (According to HUGO)	-
MGLL in Specialized Databases (According to ATLAS, GENATLAS, HORDE, IMGT, MTDB, LEIDEN and/or SWISS- PROT/TrEMBL)	-
Services (According to RZPD)	<u>Search RZPD for clones of MGEA6</u> Clone collection at the German Human Genome Project, Resource Center

- More like this

- search millions of **Web pages** with **Excite** to find other web sites related to **MGLL!**

GeneCards **Homepage** - How to **Search** or **Cite** this Database - Last **Update**: Wed Feb 25 18:23:53 Asia/Jerusalem 2004Search GeneCards for Display the GeneCard of a random gene

Display the GeneCard of a random HUGO-approved gene

The GeneCards **idea** in brief: **Mining** the Internet for biomedical knowledge and **guiding** the user to it.

Developed at the Crown Human Genome Center & Weizmann Institute of Science

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